

FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Report Date for this Batch: 26 May 2014

FMDV type O

Country: Tunisia

Period: 2014

No. of sequences: 2 (VP1)

Originator: [REDACTED] National Reference Centre for
Vesicular Diseases, Istituto Zooprofilattico Sperimentale della
Lombardia e dell'Emilia Romagna (IZSLER), Brescia, Italy.



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FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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Serotype: O	Report date: 26/05/2014
WRLFMD Ref No: TUN/1031/2014*	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00010	Checked by: D.P. King
Sender Ref: 1031 (IZSLER 134444/1)	
Location: Somaa, Tunisia	Topotype: ME-SA
Date collected: 26/04/2014	Genotype/strain: Ind-2001d
Date received by WRLFMD: 26/05/2014	Sequence filename: TUN14-AA.SEQ
Date received for sequencing: n/a	Date sequence last updated: 26/05/2014
Species: Cattle	No. of Nt determined: 639
Material used: epithelial susp	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3845
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 0 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/TUN/1054/2014*	TUN14-AB	639	637	0	99.69	0.31	ME-SA	Ind-2001d
2	O/LIB/1/2013	LIB13-01	639	632	0	98.90	1.10	ME-SA	Ind-2001d
3	O/LIB/11/2013	LIB13-11	639	632	0	98.90	1.10	ME-SA	Ind-2001d
4	O/LIB/12/2013	LIB13-12	639	632	0	98.90	1.10	ME-SA	Ind-2001d
5	O/LIB/4/2013	LIB13-04	639	632	0	98.90	1.10	ME-SA	Ind-2001d
6	O/LIB/5/2013	LIB13-05	639	632	0	98.90	1.10	ME-SA	Ind-2001d
7	O/LIB/7/2013	LIB13-07	639	632	0	98.90	1.10	ME-SA	Ind-2001d
8	O/LIB/13/2013	LIB13-13	639	631	0	98.75	1.25	ME-SA	Ind-2001d
9	O/LIB/16/2013	LIB13-16	639	631	0	98.75	1.25	ME-SA	Ind-2001d
10	O/LIB/17/2013	LIB13-17	639	631	0	98.75	1.25	ME-SA	Ind-2001d
Most Closely Related Reference Viruses									
(see http://www.wrlfmd.org/fmd_genotyping/prototypes.htm)									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BHU/3/2009	BHU09-03	639	608	0	95.15	4.85	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	582	0	91.08	8.92	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	579	0	90.61	9.39	ME-SA	Ind-2001a
4	O/UAE/4/2008	UAE08-04	636	570	0	89.62	10.38	ME-SA	Ind-2001c
5	O/IRN/31/2009	IRN09-31	639	570	0	89.20	10.80	ME-SA	PanAsia-2 ^{FAR-09}
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{TER-08}
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	565	0	88.42	11.58	ME-SA	PanAsia
8	O/IRN/8/2005	IRN05-08	639	564	0	88.26	11.74	ME-SA	PanAsia-2
9	O/PAK/16/2010	PAK10-16	639	563	0	88.11	11.89	ME-SA	PanAsia-2 ^{PUN-10}
10	O/IRN/18/2010	IRN10-18	639	562	0	87.95	12.05	ME-SA	PanAsia-2 ^{BAL-09}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.2

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Serotype: O	Report date: 26/05/2014
WRLFMD Ref No: TUN/1054/2014*	Reported by: N.J. Knowles
Batch No: WRLMEG/2014/00010	Checked by: D.P. King
Sender Ref: 1054 (IZSLER 134444/4)	
Location: Sidi Bouzid, Tunisia	Topotype: ME-SA
Date collected: 29/04/2014	Genotype/strain: Ind-2001d
Date received by WRLFMD: 26/05/2014	Sequence filename: TUN14-AB.SEQ
Date received for sequencing: n/a	Date sequence last updated: 26/05/2014
Species: Cattle	No. of Nt determined: 639
Material used: epithelial susp	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 639
RT-PCR primers: O-1C244F/EUR-2B52R	Total no. of comparisons: 3845
O-1C272F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 0 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/TUN/1031/2014*	TUN14-AA	639	637	0	99.69	0.31	ME-SA	Ind-2001d
2	O/LIB/1/2013	LIB13-01	639	634	0	99.22	0.78	ME-SA	Ind-2001d
3	O/LIB/11/2013	LIB13-11	639	634	0	99.22	0.78	ME-SA	Ind-2001d
4	O/LIB/12/2013	LIB13-12	639	634	0	99.22	0.78	ME-SA	Ind-2001d
5	O/LIB/4/2013	LIB13-04	639	634	0	99.22	0.78	ME-SA	Ind-2001d
6	O/LIB/5/2013	LIB13-05	639	634	0	99.22	0.78	ME-SA	Ind-2001d
7	O/LIB/7/2013	LIB13-07	639	634	0	99.22	0.78	ME-SA	Ind-2001d
8	O/LIB/13/2013	LIB13-13	639	633	0	99.06	0.94	ME-SA	Ind-2001d
9	O/LIB/16/2013	LIB13-16	639	633	0	99.06	0.94	ME-SA	Ind-2001d
10	O/LIB/17/2013	LIB13-17	639	633	0	99.06	0.94	ME-SA	Ind-2001d
Most Closely Related Reference Viruses									
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Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	O/BHU/3/2009	BHU09-03	639	610	0	95.46	4.54	ME-SA	Ind-2001d
2	O/OMN/7/2001 (DQ164941)	OMN01-07	639	584	0	91.39	8.61	ME-SA	Ind-2001b
3	O/KUW/3/97 (DQ164904)	KUW97-03	639	581	0	90.92	9.08	ME-SA	Ind-2001a
4	O/UAE/4/2008	UAE08-04	636	572	0	89.94	10.06	ME-SA	Ind-2001c
5	O/IRN/31/2009	IRN09-31	639	572	0	89.51	10.49	ME-SA	PanAsia-2 ^{FAR-09}
6	O/TUR/257/2008* (FMDI)	TUR08-AD	639	567	0	88.73	11.27	ME-SA	PanAsia-2 ^{TER-08}
7	O/UKG/35/2001 (AJ539141)	UKG01-35	639	567	0	88.73	11.27	ME-SA	PanAsia
8	O/IRN/8/2005	IRN05-08	639	566	0	88.58	11.42	ME-SA	PanAsia-2
9	O/PAK/16/2010	PAK10-16	639	565	0	88.42	11.58	ME-SA	PanAsia-2 ^{PUN-10}
10	O/IRN/18/2010	IRN10-18	639	564	0	88.26	11.74	ME-SA	PanAsia-2 ^{BAL-09}

nt, nucleotides

*, not a WRLFMD reference number

Assembled with Report Generator v4.2

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Report on FMDV O in Tunisia in 2014

Batch: WRLMEG/2014/00010

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 642

No Of Bootstrap Reps = 1000

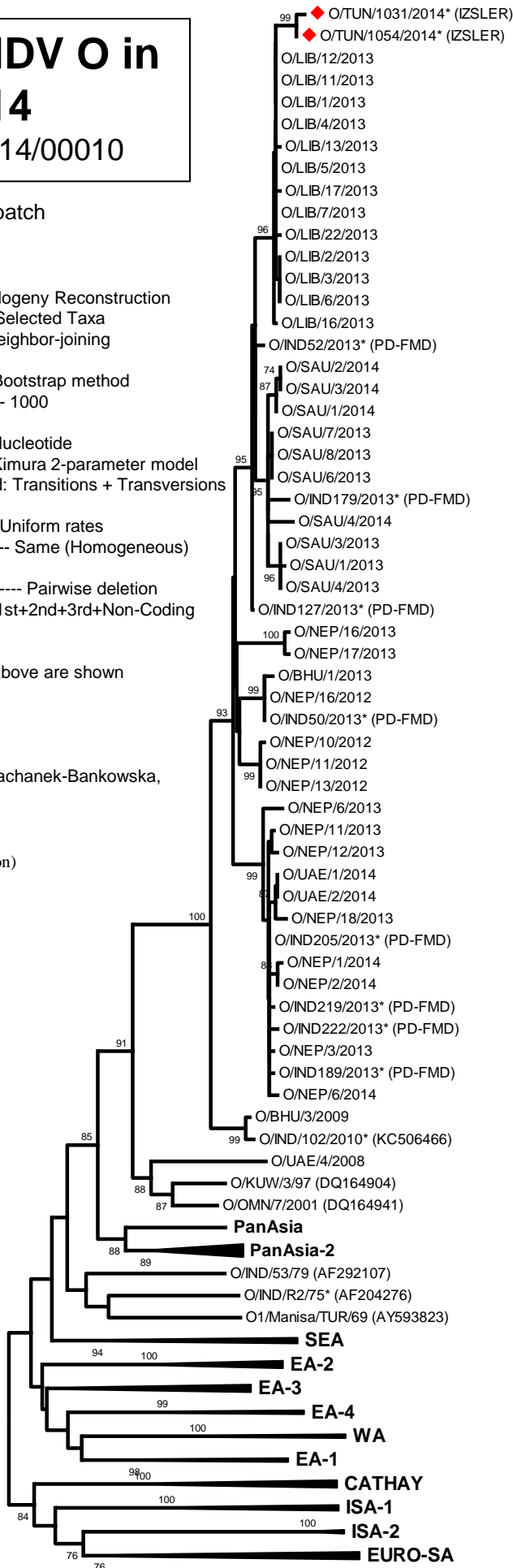
Only bootstrap values of 70% and above are shown

*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,
26 May 2014

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d

Ind-2001

ME-SA

c

a

b

0.02